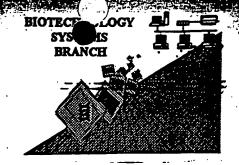
## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

09/643,755 01PE Application Serial Number:

Source:

8-30-2000 Date Processed by STIC:

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER **VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

## Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2Kcompliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

## ERROR DETECTED SUGGESTED CORRECTION

ATT	N: NEW RULES CASES:	PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE	<u>!</u>
1	_ Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line.	
		This may occur if your file was retrieved in a word processor after creating it.	
		Please adjust your right margin to .3, as this will prevent "wrapping".	
2	_ Wrapped Aminos	The amino acid number/text at the end of each line "wrapped " down to the next line.	
	,	This may occur if your file was retrieved in a word processor after creating it.	
	•	Please adjust your right margin to .3, as this will prevent "wrapping".	-
3	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces:	
4	Misaligned Amino Acid	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs	
	Numbering	between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	. •
5	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.	
		Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
6	Variable Length	Sequence(s) contain n's or Xaa's which represented more than one residue.	
		As per the rules, each n or Xaa can only represent a single residue.	
		Please present the maximum number of each residue having variable length and	
		Indicate in the (bt) feature section that some may be missing.	
7	Patentin ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid	
	•	sequence(s) Normally, Patentin would automatically generate this section from the	
		previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section	-
	•	to the subsequent amino acid sequence. This applies primarily to the mandatory <220><223>	
•		sections for Artificial or Unknown sequences.	
8	Skipped Sequences	Sequence(s) missing. If Intentional, please use the following format for each skipped sequence:	
	(OLD RULES)	(2) INFORMATION FOR SEQ ID NO:X:	
		(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTI	CS")
		(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:	
		This sequence is intentionally skipped	
		Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
9	Skipped Sequences	Sequence(s) missing. If Intentional, please use the following format for each skipped sequence.	
	(NEW RULES)	<210> sequence id number	
		<400> sequence id number	
		000	
10	Use of n's or Xaa's	Use of n's and/or Xaa's have been detected in the Sequence-Listing.	
	(NEW RULES)	Use of <220> to <223> is MANDATORY if n's or Xaa's are present.	
		In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11	Use of <213>Organism	Sequence(s) are missing this mandatory field or its response.	
	(NEW RULES)		
/	11	Sequence(s) are missing the <220>Feature and associated headings.	
12 <u>V</u>	Use of <220>Feature	Sequence(s) 7 are missing the <220>Feature and associated headings.	
	(NEW RULES)	OSC OF 1220 TO 1220 TO WARTON TO THE 12 TO CONCONTROL OF CHINDREN	
		Please explain source of genetic material in <220> to <223> section.	
		(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new	Rules)
13	Patentin ver. 2.0 "bug"	Please do not use "Copy to Disk" function of Patentin version 2.0. This causes a corrupted	• •
	Ţ	file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).	
		Instead, please use "File Manager" or any other means to copy file to floppy disk.	

OIPE

RAW SEQUENCE LISTING DATE: 08/30/2000 PATENT APPLICATION: US/09/643,755 TIME: 14:32:19

Input Set : A:\Sequence

Output Set: N:\CRF3\08302000\1643755.raw

Does Not Comply Corrected Diskette Needed

see p.4,6

```
4 <110> APPLICANT: van Rooijen, Gijs
               Keon, Richard Glenn
      5
               Boothe, Joseph
               Shen, Yin
     10 <120> TITLE OF INVENTION: Commercial Production of Chymosin in Plants
     12 <130> FILE REFERENCE: 9369-153
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/643.755
C--> 15 <141> CURRENT FILING DATE: 2000-08-23
     17 <160> NUMBER OF SEQ ID NOS: 4
     19 <170> SOFTWARE: PatentIn Ver. 2.0
     21 <210> SEQ ID NO: 1
     22 <211> LENGTH: 1173
     23 <212> TYPE: DNA
     →24 <213> ORGANISM: Bovine
     26 <220> FEATURE:
     27 <221> NAME/KEY: CDS
     28 <222> LOCATION: (1)..(1173)
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   _{-} ^{32} Met Asn Phe Leu Lys Ser Phe Pro Phe Tyr Ala Phe Leu Cys Phe Gly
     33 1
                           5
                                                 10
     35 caa tac ttc gtt gct gtt act cac gct gct gag atc acc cgc att cct
     36 Gln Tyr Phe Val Ala Val Thr His Ala Ala Glu Ile Thr Arg Ile Pro 37 20 25 30
     39 ctc tac aaa ggt aag tct ctc cgt aag gcg ctg aag gaa cat gga ctt 40 Leu Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu 41 35 40 45
     43 cta gaa gac ttc ttg cag aaa caa cag tat ggc atc agc agc aag tac
     44 Leu Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr
     47 tcc ggc ttc ggt gaa gtt gct agc gtg cca ctt acc aac tac ctt gat
48 Ser Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp
49 65 70 75 80
                                                                                  240
                                                   75
     51 agt caa tac ttt ggg aag atc tac ctc gga acc ccg cct caa gag ttc
                                                                                  288
     52 Ser Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe
                          85
     55 acc gtt ctc ttt gat act ggt tcc tct gac ttc tgg gtt ccc tct atc
     56 Thr Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile
                    100
                                        105
     59 tac tgc aag agc aat gcc tgc aag aac cac caa aga ttc gat ccg aga
                                                                                  384
    60 Tyr Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg
61 115 120 125
                                                            125
     63 aag tog toe acc tte cag aac tta ggc aaa coc ttg tot ata cac tac
     64 Lys Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr
          130
                                  135
                                                        140
     67 ggt aca ggt agc atg caa gga atc tta ggc tat gat acc gtc act gtc
     68 Gly Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val
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RAM SEQUENCE LISTING DATE: 08/30/2000 PATENT APPLICATION: US/09/643,755 TIME: 14:32:19

Input Set : A:\Sequence
Output Set: N:\CRF3\08302000\1643755.raw

155 71 tcc aac att gtg gac att caa cag aca gta gga ctt agc acc caa gaa 72 Ser Asn Ile Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu 73 165 170 175 75 cca ggt gat gtc ttc acc tat gca gaa ttc gat ggc atc ctt ggt atg 76 Pro Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met 190 180 185 79 gca tac cca tcg ctc gcg tca gag tac tcg ata cct gtg ttt gac aac 80 Ala Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn 81 195 200 205 83 atg atg aac cga cac cta gta gct caa gac ttg ttc tcg gtt tac atg 84 Met Met Asn Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met 220 85 210 215 87 gac agg aat ggc cag gag agc atg ctc acg ctt gga gct att gat cca 88 Asp Arg Asn Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro 230 235 89 225 91 tcc tac tac aca gga tct ctt cac tgg gtt cca gtc act gtg cag cag 92 Ser Tyr Tyr Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln 93 245 250 255 95 tac tgg caa ttc act gtg gac agt gtc acc atc agc ggt gtg gtt gtt 96 Tyr Trp Gln Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val 270 260 265 99 gca tgt gaa ggt gga tgt caa gct atc ttg gat acc ggt acg tcc aag 100 Ala Cys Glu Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys 101 275 280 285 103 ctg gtc gga cct agc agc gac att ctc aac att cag caa gct att gga 104 Leu Val Gly Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly 105 290 295 300 107 gcc aca cag aac cag tac ggt gag ttt gac ata gat tgc gac aac ctt 108 Ala Thr Gln Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu 109 305 310 315 320 111 agc tac atg cct aca gtt gtc ttt gag atc aac ggc aag atg tac cca 112 Ser Tyr Met Pro Thr Val Val Phe Glu Ile Asn Gly Lys Met Tyr Pro 1008 325 330 115 ctg acc ccc tcc gcc tat acc agc cag gat caa ggg ttc tgc acc agt 116 Leu Thr Pro Ser Ala Tyr Thr Ser Gln Asp Gln Gly Phe Cys Thr Ser 117 340 345 350 119 gga ttc cag agt gag aac cat tcc cag aaa tgg atc ttg gga gat gtg 120 Gly Phe Gln Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val 1104 360 355 123 tto att ogt gag tac tac ago gto ttt gac agg gcc aac aac ctc gtt 124 Phe Ile Arg Glu Tyr Tyr Ser Val Phe Asp Arg Ala Asn Asn Leu Val 375 125 370 127 ggg cta gct aaa gca atc tga 128 Gi: Leu Ala Lys Ala Ile 129 385 390 1173 129 385 132 <210> SEQ ID NO: 2

133 <211> LENGTH: 390 134 <212> TYPE: PRT RAW SEQUENCE LISTING DATE: 08/30/2000 PATENT APPLICATION: US/09/643,755 TIME: 14:32:19

Input Set : A:\Sequence

Output Set: N:\CRF3\08302000\1643755.raw

135 <213> ORGANISM: Bovine 137 <400> SEQUENCE: 2 138 Met Asn Phe Leu Lys Ser Phe Pro Phe Tyr Ala Phe Leu Cys Phe Gly 139 1 5 10 141 Gln Tyr Phe Val Ala Val Thr His Ala Ala Glu Ile Thr Arg Ile Pro 142 20 25 30 144 Leu Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu 145 35 40 45 147 Leu Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr 148 50 55 60 150 Ser Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp 151 65 70 75 80 153 Ser Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe 154 85 90 95 156 Thr Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile 157 100 105 110 159 Tyr Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg 160 115 120 125 162 Lys Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr 163 130 135 140 165 Gly Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val 166 145 168 Ser Asn Ile Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu 169 165 170 175 171 Pro Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met 172 180 185 190 174 Ala Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn 175 195 200 205 177 Met Met Asn Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met 178 210 215 220 180 Asp Arg Asn Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro 181 225 230 240 183 Ser Tyr Tyr Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln 184 245 250 250 186 Tyr Trp Gln Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val 187 260 265 270 189 Ala Cys Glu Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys 190 275 280 285 192 Leu Val Gly Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly 193 290 295 300 195 Ala Thr Gln Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu 196 305 310 315 320 198 Ser Tyr Met Pro Thr Val Val Phe Glu Ile Asn Gly Lys Met Tyr Pro 199 325 330 335 201 Leu Thr Pro Ser Ala Tyr Thr Ser Gln Asp Gln Gly Phe Cys Thr Ser 202 340 345 204 Gly Phe Gln Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val 205 355 360 365 355 207 Phe Ile Arg Glu Tyr Tyr Ser Val Phe Asp Arg Ala Asn Asn Leu Val

RAW SEQUENCE LISTING PATENT APPLICATION: US/09/643,755 DATE: 08/30/2000 TIME: 14:32:19

Input Set : A:\Sequence

Output Set: N:\CRF3\08302000\1643755.raw

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380
       370
208
210 Gly Leu Ala Lys Ala Ile
211 385
214 <210> SEQ ID NO:
                                                                            More specific
source of genetic
material in the
215 <211> LENGTH: 3957
216 <212> TYPE: DNA
217 <213> ORGANISM: Artificial Sequence
219 <220> FEATURE:
220 <221> NAME/KEY: CDS
221 <222> LOCATION: (1554)..(2726)
224 <223> OTHER INFORMATION: Description of Artificial Sequence Figure 2
226 <400> SEQUENCE: 3
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                                                                             artificial sequence
229 tggtttttta cctctattta aaggggtttt ccacctaaaa attctggtat cattctcact 120
231 tracttgtta ctttaatttc tcataatctt tggttgaaat tatcacgctt ccgcacacga 180
233 tatecetaca aatttattat ttgttaaaca ttttcaaace gcataaaatt ttatgaagte 240
235 cogtotatot ttaatgtagt ctaacatttt catattgaaa tatataattt acttaatttt 300
                                                                               See #12 00
237 agcgttggta gaaagcataa agatttatto ttattottot toatataaat gtttaatata 360
239 caatataaac aaattettta eettaagaag gattteecat titatatitt aaaaatatat 420
241 ttatcaaata tttttcaacc acgtaaatct cataataata agttgtttca aaagtaataa 480
                                                                              Error Summery
243 aatttaactc cataatttt ttattcgact gatcttaaag caacacccag tgacacaact 540
245 agccattttt ttctttgaat aaaaaaatcc aattatcatt gtatttttt tatacaatga 600
247 aaatttcacc aaacaatcat ttgtggtatt tctgaagcaa gtcatgttat gcaaaattct 660
249 ataattccca tttgacacta cggaagtaac tgaagatctg cttttacatg cgagacacat 720
251 cttctaaagt aattttaata atagttacta tattcaagat ttcatatatc aaatactcaa 780
253 tattacttot aaaaaattaa ttagatataa ttaaaatatt acttttttaa ttttaagttt 840
255 aattgttgaa tttgtgacta ttgatttatt attctactat gtttaaattg ttttatagat 900
257 agtttaaagt aaatataagt aatgtagtag agtgttagag tgttacccta aaccataaac 960
259 tataacattt atggtggact aattttcata tatttcttat tgcttttacc ttttcttggt 1020
261 atgtaagtcc gtaactagaa ttacagtggg ttgccatggc actctgtggt cttttggttc 1080
263 atgcatgggt cttgcgcaag aaaaagacaa agaacaaaga aaaaagacaa aacagagaga 1140
265 caaaacgcaa tcacacaacc aactcaaatt agtcactggc tgatcaagat cgccgcgtcc 1200
267 atgtatgtct aaatgccatg caaagcaaca cgtgcttaac atgcacttta aatggctcac 1260
269 ccatctcaac ccacacaaa acacattgcc tttttcttca tcatcaccac aaccacctgt 1320
 271 atatattcat tetetteege caceteaatt tetteaette aacacaegte aacetgeata 1380
 273 tgcgtgtcat cccatgccca aatctccatg catgttccaa ccaccttctc tcttatataa 1440
 275 tacctataaa tacctctaat atcactcact tetttcatca tecatecate cagagtacta 1500
 278
 281 aac ttc ctt aag tct ttc cct ttc tac gct ttc ctt tgt ttc ggt caa
                                                                        1604
 282 Asn Phe Leu Lys Ser Phe Pro Phe Tyr Ala Phe Leu Cys Phe Gly Gln
                                     10
 285 tac ttc gtt gct gtt act cac gct gct gag atc acc cgc att cct ctc 286 Tyr Phe Val Ala Val Thr His Ala Ala Glu Ile Thr Arg Ile Pro Leu
                                 . 25
 289 tac aaa ggt aag tot oto ogt aag gog otg aag gaa oat gga ott ota
290 Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu Leu
             20
                                                                        1700
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Sheet.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/643,755

DATE: 08/30/2000 TIME: 14:32:19

Input Set : A:\Sequence
Output Set: N:\CRF3\08302000\1643755.raw

				-													
291		35					40					45					
202	gaa	~~~	ttc	tta	cag	aaa	caa	cag	tat	ggc	atc	agc	agc	aag	tac	tcc	1748
294	Glu	Asp	Phe	Leu	Gln	Lys	Gln	Gln	Tyr	Gly	Ile	Ser	Ser	Lys	Tyr	501	
205	50					55					90					0.5	
207		ttc	aat	gaa	gtt	qct	agc	gtg	cca	ctt	acc	aac	tac	ctt	gat	agt	1796
298	Glv	Phe	Glv	Ğlu	Val	Ála	Ser	Val	Pro	Leu	Thr	asn	Tyr	Leu	vəħ	Ser	
200					70					/ >							1011
201	caa	tac	ttt	PPP	aag	atc	tac	ctc	gga	acc	ccg	cct	caa	gag	ttc	acc	1844
302	Gln	Tyr	Phe	Gly	Lys	Ile	Tyr	Leu	Gly	Thr	Pro	Pro	Gln	GIU	Phe	Thr	
202				25					90					,,			1000
305	att	ctc	ttt	gat	act	ggt	tcc	tct	gac	ttc	tgg	gtt	ccc	tct	atc	tac	1892
306	Val	Leu	Phe	ÅSP	Thr	Gly	Ser	Ser	Asp	Phe	Trp	Val	PIO	Ser	He	Tyr	
307			100					105					110				1010
200	tac	аач	agc	aat	gcc	tgc	aag	aac	cac	caa	aga	ttc	gat	ccg	aga	aag	1940
310	CVS	Lvs	Ser	Asn	Ala	Cys	Lys	Asn	His	Gln	Arg	Pile	Asp	Pro	Arg	гåа	
211		115					120					127					1000
212	tcq	tcc	acc	ttc	cag	aac	tta	ggc	aaa	ccc	ttg	tct	ata	cac	tac	ggt	1988
314	Ser	Ser	Thr	Phe	Gln	Asn	Leu	Gly	Lys	Pro	Leu	Ser	He	His	Tyr	Gry	
215	120					125					140					747	2026
317	aca	ggt	agc	atg	caa	gga	atc	tta	ggc	tat	gat	acc	gtc	act	gtc	tcc	2036
318	Thr	Gly	Ser	Met	Gln	Gly	Ile	Leu	Gly	LÀL	Asp	Thr	Val	inr	* 441	Ser	
210					150					722					100		2084
321	aac	att	gtg	gac	att	çaa	cag	aca	gta	gga	ctt	agc	acc	caa	gaa	CCa	2004
322	Asn	Ile	Val	Asp	Ile	Gln	Gln	Thr	Val	Gly	Leu	Ser	Thr	GIII	GIU	PIO	
323				165					1/0					1/3			2132
325	ggt	gat	gtc	ttc	acc	tat	gca	gaa	ttc	gat	ggc	atc	CLL	ggt	Wat	λla	2132
326	Gly	Asp	Val	Phe	Thr	Tyr	Ala	Glu	Phe	Asp	GIY	116	190	GIŞ	met	VIG	
327			180					185				-+-		~~	220	atσ	2180
329	tac	cca	tcg	ctc	gcg	tca	gag	tac	tcg	ata	CCL	gry	Dho	yac Aan	A c n	Met	2200
330	Tyr	Pro	Ser	Leu	Ala	Ser	Glu	Tyr	Ser	11e	PIO	205	rne	vaħ	N311	ne c	
331		195					200				++-		a++	tac	ato	gac	2228
333	atg	aac	cga	cac	cta	gta	gct	caa	gac	tty	Dho	For	Val	Tur	Met	Agn	
		Asn	Arg	His	Leu	Val	Ala	GID	ASP	Leu	220	261	141	111	1100	225	
335	210					215				a++		act	att	gat	cca		2276
337	agg	aat	ggc	cag	gag	agc	atg	CCC	The	tou	Glv	Ala	Tle	Asp	Pro	Ser	
	Arg	Asn	Gīā	Gin	Glu	Ser	Met	Leu	1111	235	GIY	ALG			240		
339					230 tct			+ ~ ~	att		atc	act	ata	cag	cag	tac	2324
341	tac	tac	aca	gga	Ser	TOU	Uic	Trn	Val	Pro	Val	Thr	Val	Gln	Gln	Tyr	
	Tyr	Tyr	Thr	245	Ser	rea	nis	ııp	250					255		_	
343				243	gtg	<b>430</b>	agt	ato		atc	aσc	aat	ata	qtt	gtt	gça	2372
345	tgg	Caa	Dha	act mb-	Val	ren	Car	Val	Thr	Tle	Ser	Ğĺv	Val	Val	Val	Ala	
	irp	GIn	260	THE	Val	чэр	361	265					270				
347			200		tgt	c 2 2	act	atc	tta	σat.	acc	aat	acq	tcc	aag	ctg	2420
349	Cur	yaa Cl.	990	61:	Cys	Gin	Ala	Ile	Leu	ASD	Thr	Ğĺv	Thr	Ser	Lys	Leu	
350		275		GTĀ	Cys	GIII	280					285			-		
252	a+ a		cot	age	agc	gac	att	ctc	aac	att	cag	caa	gct	att	gga	gcc	2468
354	Val	99ª	Dro	Spr	Ser	Asp	Tle	Leu	Asn	Ile	Gln	Gln	Ala	Ile	Gly	Ala	
	290	GLY	-10	501	501	295					300					305	
,,,	230																

O9/64) 755

Missing modatory (220) and

(210> 4
(211> 390
(212> PRT
(213> Artificial Sequence

On Error Summary Sizet.

<400>4 Met Asn Phe Leu Lys Ser Phe Pro Phe Tyr Ala Phe Leu Cys Phe Gly

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/643,755

DATE: 08/30/2000 TIME: 14:32:20

Input Set : A:\Sequence
Output Set: N:\CRP3\08302000\1643755.raw

L:14 M:270 C: Current Application Number differs, Replaced Application Number L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:429 M:258 W: Mandatory Feature missing, <220> FEATURE: L:429 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

Application No. <u>09/643755</u>

## NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUMBER OF THE PROPERTY O

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.	
2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).	
3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e	).
4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached marked-up copy of the "Raw Sequence Listing."	
5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).	•
6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).	
7. Other: ————————————————————————————————————	
Applicant must provide:	
An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"	
An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification	
A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)	
For questions regarding compliance with these requirements, please contact:	
For Rules Interpretation, call (703) 308-1123 For CRF submission help, call (703) 308-4212 For Patentin software help, call (703) 308-6856	

Please return a copy of this notice with your response.